needs to be studied in preanthesis, as these hairs shrivel during anthesis. The presence of this hair tuft in the ventral anthers could be plesiomorphic in *Burmeistera*, as it is also present in the related genera *Centropogon, Lobelia*, and *Syphocampylus.* We propose that the ebracteate peduncle is a potentially phylogenetically informative character within *Burmeistera*.

P0806 – Poster

Flora of the State Park El Faro and its potential use

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The State Park of 'El Faro', located in Tlalmanalco, State of Mexico, is part of the Ecological Reserve of the Sierra Nevada, which consists of different biological corridors, product of the principal reason of the enormous biological richness of our country: the meeting of two kingdoms biogeograficos (the Neártica and the Neotropical). Nevertheless, in spite of possessing legal protection for the conservation of these corridors there has been observed in the last years an intensive growth of the human settlements that they find around it. This demographic growth attracts undoubtedly direct consequences in the ecosystem of the reserve principally in loss of biodiversity. The Sierra Nevada headquarter of 'El Faro' and of the historical volcanoes Popocatépetl and Iztaccíhuatl, it constitutes a very important area for the capital of Mexico for the mass of oxygen that it provides to it and for constituting one of the most important reserves of water, since it provides to great part of the east of the metropolitan zone. Nowadays faced with the imminent deforestation that we face for diverse social factors such as poverty, lack of employment, immoderate felling etc., it is necessary to have information about the condition of the flora of the state park 'El Faro' and to contribute to the analysis of the local vegetation, as well as to help to the inventory of its biodiversity. Periodic samplings were made in the park with the intention of contrasting and monitoring the variety of existing species. Likewise there decided the potential use of flora of the park. The assignment as Natural Protected Area, of 'El Faro', has as principal aim to protect and preserve the natural environment, in order to support the balance and the continuity of the ecological processes, and of its elements, by means of the implementation of protection programs, managing and environmental education and scientific research; to assure the use and sustainable utilization of the resources for the future generations.

P0808 – ePoster

Genetic diversity and phylogeography of wild-sown and cultivated coconuts (*Cocos nucifera* L.)

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The coconut (*Cocos nucifera* L.) is a pantropical strand plant, colonizing sandy insular beaches in the humid tropics. *Cocos* is a monotypic genus in the Cocoseae tribe (18/ca. 200 spp.) within the Arecaceae family. Phylogenetic studies support its sister relationship to *Syagrus*, a Neotropical genus, sharing a common ancestor about 35 MYBP, though the crown group age of *Cocos* is about 11 MYBP. Fossil evidence indicates that members of the *Cocos* lineage were present in South America, India, New Zealand and Australia. Coconuts are adapted to drift-dispersal by ocean currents; however, human activities both historically and today have also aided its spread and impacted its phenotypic and genetic structure. Coconuts are traditionally classified as 'Talls' or 'Dwarfs' based on tree habit. Morphological examination reveal two predominant fruit types, attributed to Polynesian terminology: *niu kafa* are characterized by their elongated, triangular fruits with large proportion of fibrous husk and *niu vai,* whose fruits are rounded with large proportion of liquid endosperm. The niu kafa form is interpreted as the naturally evolved coconut, under natural selection for dissemination by sea currents whilst the niu vai form evolved from domestication under human selection for greater volume of delicious coconut water. Here we investigate the genetic diversity of coconuts, the impact of domestication, introgression and the taxonomic implications for this species. We used polymorphic microsatellite markers on 1322 coconut samples representing phenotypic and genetic variation worldwide to examine the geographical location of the center(s) of domestication and its progenitors. Bayesian analyses of population structure revealed two major subpopulations corresponding to the Pacific and Indo–Atlantic oceanic regions. Haplotype networks based on chloroplast and nuclear markers are used as a complementary dataset to examine the coconut's phylogeography.

P0809 – ePoster

Population structure of the A-genome group in *Glycine* subg. *Glycine* (Fabaceae)

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Sister to the cultivated soybean, *Glycine* subg. *Glycine* contains several diploid genome groups of species native to Australia and Papua New Guinea. Each genome group is defined by its species being interfertile and has been validated as monophyletic with molecular study. Many of these groups contain species contributing to the *Glycine* polyploid complex. The A-genome is the largest genome group and consists of about seven species. *G. syndetika, G. canescens*, and *G. clandestina* are the three A-genome representatives that contribute to the polyploid complex. Due in part to *Glycine* subg. *Glycine* being predominantly autogamous with common cleistogamy, population structure of the A-genome species has been poorly understood. Such structure is important for elucidating the formation of the entire polyploid complex. To uncover population structure we analyzed